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RAW SEQUENCE LISTING

DATE: 04/26/2002

PATENT APPLICATION: US/09/697,186A

TIME: 11:52:32

Input Set : A:\48530048.app

Output Set: N:\CRF3\04262002\I697186A.raw

ENTERED

3 <110> APPLICANT: YOKOYAMA, SIGEYUKI
 4 HOSEKI, JUN
 5 YANO, TAKATO
 6 KOYAMA, YOSHINORI
 7 KURAMITSU, SEIKI
 8 KAGAMIYAMA, HIROYUKI
 10 <120> TITLE OF INVENTION: MUTANT KANAMYCIN NUCLEOTIDYLTRANSFERASE AND A METHOD
 11 OF SCREENING THERMOPHILIC BACTERIA USING THE SAME
 13 <130> FILE REFERENCE: 04853.0048-00000
 15 <140> CURRENT APPLICATION NUMBER: 09/697,186A
 C--> 16 <141> CURRENT FILING DATE: 2002-04-11
 18 <150> PRIOR APPLICATION NUMBER: JP 309616/1999
 19 <151> PRIOR FILING DATE: 1999-10-29
 21 <160> NUMBER OF SEQ ID NOS: 20
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 253
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: Mutant enzyme
 32 obtained by introduction of point mutation into
 33 wild type KNT gene of Staphylococcus aureus and
 34 its expression
 36 <400> SEQUENCE: 1
 37 Met Asn Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val
 38 1 5 10 15
 40 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys
 41 20 25 30
 43 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr
 44 35 40 45
 46 Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu Phe
 47 50 55 60
 49 Ser His Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe Tyr
 50 65 70 75 80
 52 Ser Glu Glu Ile Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp Trp
 53 85 90 95
 55 Pro Leu Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp Ser
 56 100 105 110
 58 Gly Gly Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala
 59 115 120 125
 61 Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe
 62 130 135 140

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64 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr
65 145          150          155          160
67 Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu
68          165          170          175
70 Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu
71          180          185          190
73 Thr Glu Ala Val Lys Gln Ser Asp Leu Pro Ser Gly Tyr Asp His Leu
74          195          200          205
76 Cys Gln Phe Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu Leu
77          210          215          220
79 Glu Ser Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu Arg
80 225          230          235          240
82 His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe
83          245          250
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87 <211> LENGTH: 253
88 <212> TYPE: PRT
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Description of Artificial Sequence: Mutant enzyme
93     obtained by introduction of point mutation into
94     wild type KNT gene of Staphylococcus aureus and
95     its expression
97 <400> SEQUENCE: 2
98 Met Lys Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val
99  1      5      10      15
101 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys
102      20      25      30
104 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr
105      35      40      45
107 Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Gly Ala Glu Phe
108      50      55      60
110 Ser Tyr Glu Trp Thr Thr Gly Glu Trp Lys Ala Glu Val Asn Phe Tyr
111 65      70      75      80
113 Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Arg Val Glu Ser Asp Trp
114      85      90      95
116 Pro Leu Thr His Gly Arg Phe Phe Ser Ile Leu Pro Ile Tyr Asp Pro
117      100     105     110
119 Gly Gly Tyr Phe Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala
120      115     120     125
122 Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe
123      130     135     140
125 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr
126 145     150     155     160
128 Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu
129      165     170     175
131 Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu
132      180     185     190
134 Thr Glu Ala Val Lys Gln Pro Asp Leu Pro Ser Gly Tyr Asp His Leu

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135          195          200          205
137 Cys Gln Leu Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu Leu
138          210          215          220
140 Glu Ser Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu Arg
141 225          230          235          240
143 His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe
144          245          250
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150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Description of Artificial Sequence: Mutant enzyme
154     obtained by introduction of point mutation into
155     wild type KNT gene of Staphylococcus aureus and
156     its expression
158 <400> SEQUENCE: 3
159 Met Lys Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val
160  1          5          10          15
162 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys
163          20          25          30
165 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr
166          35          40          45
168 Ser Asp Ile Glu Met Met Cys Val Leu Ser Thr Glu Gly Val Glu Phe
169          50          55          60
171 Ser Tyr Glu Trp Thr Thr Gly Glu Trp Lys Ala Glu Val Asn Phe Tyr
172 65          70          75          80
174 Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Arg Val Glu Pro Asp Trp
175          85          90          95
177 Pro Leu Thr His Gly Arg Phe Phe Ser Ile Leu Pro Ile Tyr Asp Pro
178          100         105         110
180 Gly Gly Tyr Phe Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala
181          115         120         125
183 Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe
184          130         135         140
186 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr
187 145         150         155         160
189 Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu
190          165         170         175
192 Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu
193          180         185         190
195 Thr Glu Ala Val Lys Gln Pro Asp Leu Pro Pro Gly Tyr Val Gln Leu
196          195         200         205
198 Cys Gln Leu Val Met Ser Gly Gln Leu Ser Asp Pro Glu Lys Leu Leu
199          210         215         220
201 Glu Ser Leu Glu Asn Phe Trp Asn Gly Val Gln Glu Trp Ala Glu Arg
202 225         230         235         240
204 His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe
205          245         250

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Input Set : A:\48530048.app

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211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer for
215 PCR amplification
217 <400> SEQUENCE: 4
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221 <210> SEQ ID NO: 5
222 <211> LENGTH: 35
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer for
228 PCR amplification
230 <400> SEQUENCE: 5
231 gactgtacgc tgcagcgtaa ccaacatgat taaca 35
234 <210> SEQ ID NO: 6
235 <211> LENGTH: 35
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer for
241 PCR amplification
243 <400> SEQUENCE: 6
244 gactgtacgg aattcgagct cgagcaaatac taaaa 35
247 <210> SEQ ID NO: 7
248 <211> LENGTH: 35
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer for
254 subcloning of WT
256 <400> SEQUENCE: 7
257 gactgtacgc atatgaatgg accaataata atgac 35
260 <210> SEQ ID NO: 8
261 <211> LENGTH: 35
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer for
267 subcloning of KT3-11 and HTK
269 <400> SEQUENCE: 8
270 gactgtacgc atatgaaagg accaataata atgac 35
273 <210> SEQ ID NO: 9
274 <211> LENGTH: 35
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence

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279 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer for subcloning
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286 <211> LENGTH: 759
287 <212> TYPE: DNA
288 <213> ORGANISM: Staphylococcus aureus
290 <220> FEATURE:
291 <221> NAME/KEY: CDS
292 <222> LOCATION: (1)..(759)
294 <400> SEQUENCE: 10
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297 1 5 10 15
299 cat gaa att aag gaa cga ata ttg gat aaa tat ggg gat gat gtt aag 96
300 His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys
301 20 25 30
303 gct att ggt gtt tat ggc tct ctt ggt cgt cag act gat ggg ccc tat 144
304 Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr
305 35 40 45
307 tcg gat att gag atg atg tgt gtc atg tca aca gag gaa gca gag ttc 192
308 Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu Phe
309 50 55 60
311 agc cat gaa tgg aca acc ggt gag tgg aag gtg gaa gtg aat ttt gat 240
312 Ser His Glu Trp Thr Gly Glu Trp Lys Val Glu Val Asn Phe Asp
313 65 70 75 80
315 agc gaa gag att cta cta gat tat gca tct cag gtg gaa tca gat tgg 288
316 Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp Trp
317 85 90 95
319 ccg ctt aca cat ggt caa ttt ttc tct att ttg ccg att tat gat tca 336
320 Pro Leu Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp Ser
321 100 105 110
323 ggt gga tac tta gag aaa gtg tat caa act gct aaa tcg gta gaa gcc 384
324 Gly Gly Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala
325 115 120 125
327 caa acg ttc cac gat gcg att tgt gcc ctt atc gta gaa gag ctg ttt 432
328 Gln Thr Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe
329 130 135 140
331 gaa tat gca ggc aaa tgg cgt aat att cgt gtg caa gga ccg aca aca 480
332 Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr
333 145 150 155 160
335 ttt cta cca tcc ttg act gta cag gta gca atg gca ggt gcc atg ttg 528
336 Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu
337 165 170 175
339 att ggt ctg cat cat cgc atc tgt tat acg acg agc gct tcg gtc tta 576
340 Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu
341 180 185 190
343 act gaa gca gtt aag caa tca gat ctt cct tca ggt tat gac cat ctg 624

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date